OIPE

RAW SEQUENCE LISTING   DATE: 06/27/2002
PATENT APPLICATION: US/09/899,634B   TIME: 13:06:28

Input Set : A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt
Output Set: N:\CRF3\06272002\I899634B.raw

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      3 <110> APPLICANT: Thomas Buhler; Reto Andreas Gadient; Reinhard Korn; Rao Movva
      5 <120> TITLE OF INVENTION: pCAR and its uses
      7 <130> FILE REFERENCE: 4-31499A
C-->  9 <140> CURRENT APPLICATION NUMBER: US/09/899,634B
C-->  9 <141> CURRENT FILING DATE: 2002-06-17
      9 <160> NUMBER OF SEQ ID NOS: 12
     11 <170> SOFTWARE: PatentIn version 3.1
     13 <210> SEQ ID NO: 1
     14 <211> LENGTH: 4286
     15 <212> TYPE: DNA
C--> 16 <213> ORGANISM: Artificial/Unknown
     18 <220> FEATURE:
     19 <221> NAME/KEY: CDS
     20 <222> LOCATION: (3229)..(4014)
     21 <223> OTHER INFORMATION: delta pCAR gene
     24 <400> SEQUENCE: 1
     25 cggtgcgggc ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat    60
     27 taagttgggt aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgcca   120
     29 agttgggatc tttgcattgg cccacggctc tcaggatggg gatgctcccc ttcagcaccc   180
     31 ggttcccctt ggaaactgat ggtcctggct ctgtggcatg gcagtggcac tgtgaggagc   240
     33 ccctaccagc agcacacagt gggtttggca ctgccacgct ccggatgccg cgctctgatc   300
     35 caaccccata atcaagggaa cccgaattgc cccatcattg cccccaccac ccccatcctg   360
     37 ccgggccctc acaccccacg ctgccttgtg gtgacattcc cagcccaaa cccacggctt   420
     39 catggctacc gcggggcatt tcccattgcc gccccattat cagctctgca cacctcccgc   480
     41 tgtacccatg cctcgtggct gcccttcttt gacgtataat cttctaatta tacccggcc   540
     43 ttgtcaaagt ggagcacaaa cgttaattaa ttccccagca ggcaggtaat taacagtgtg   600
     45 actccctttt tgctgcgagt ggggctgata cagagagatg tggcactatg gagcccacgg   660
     47 ggtcctggca ctgggtgccc acggaggtcc ccatgtgctg cagtgtcacc gcctccgagg   720
     49 tgacagtatt gtccctgcgg tgtccctgca gctcagctct gtccacaggg ccacctccag   780
     51 tttggagggg acacaatgca gccccgatgc aacccatcct cgcagcatcc caggggacaaa  840
     53 gaccccactg caagaccgca cacagggctg ggtcccgctc ccctaatatc tacagtgctt   900
     55 ttgcatggcc ccttaatcaa tgcagttaat cagcatgcgc tcatgcaccg ctctggagct   960
     57 gcaaagcccc tcgcagcgct gctcaccaac accgcgcacc gccccggccc agcctgcagc  1020
     59 acgcgctgca aacaggaaag aaacaaaata ttgcccaaat gtaggcaaag gcattcggct  1080
     61 gccttgacct ccgccgggcc gggccctgcc tgactcagct ccttactcag cgctcgcttc  1140
     63 ctccctccgg ctgccaccgc cgcagcgcac accctgacaa agagtggccc ttaacgggct  1200
     65 ctgaggtgca cccagcagtg cactcagcag tccaagggcc ggcctggagg tttgcaccgc  1260
     67 tacgtgctga cattagcatt gaacttggcc ctgggtagtg ctgcaggccg ggcggggtgg  1320
     69 gtgtagagag tgcagcgcgc gttgcacccg gtgccccttc ccctcccttg catcccagca  1380
     71 ggctgcaccc cagcaccagg cccgtgcatg catgctcctg gtgttattgc agcctggtgc  1440
     73 atgcatcgt cttagtggtg cagcgctgtg catgcatcct ccttggtgtg tagcagctta  1500
     75 gtgcatgcat acccctcggt gttattgctg ctctgtgcac gcacgctcat tgtatcactt  1560
     77 catcccagtg catgcactca cactggagcg attgctgctc ggtgcacgca cactcattgt  1620
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 79 atcacgtcag ctcagtggct gcacgcacac cggtgttatt gctgctcggt gcgtgcatgc   1680
 81 acatcagtgt cgctgcagct cagtgcatgc acgctcattg cccatcgcta tccctgcctc   1740
 83 tcctgctggc gctccccggg aggtgacttc aaggggaccg caggaccacc tcggggggtgg  1800
 85 ggggagggct gcacacgcgg accccgctcc ccctccccaa caaagcactg tggaatcaaa   1860
 87 aaggggggag gggggatgga ggggcgcgtc acaccccgc cccacaccct cacctcgagg     1920
 89 tgagccccac gttctgcttc actctcccca tctccccccc ctccccaccc ccaattttgt    1980
 91 atttatttat ttttaatta ttttgtgcag cgatgggggc ggggggggggg ggggcgcgcg    2040
 93 ccaggcgggg cggggcgggg cgaggggcgg ggcggggcga ggcggagagg tgcggcggca    2100
 95 gccaatcaga gcggcgcgct ccgaaagttt ccttttatgg cgaggcggcg cgcggcggcgg   2160
 97 ccctataaaa agcgaagcgc gcggcgggcg ggagtcgctg cgttgccttc gccccgtgcc    2220
 99 ccgctccgcg ccgcctcgcg ccgcccgccc cggctctgac tgaccgcgtt actcccacag    2280
101 gtgagcgggc gggacggccc ttctcctccg ggctgtaatt agcgcttggt ttaatgacgg    2340
103 ctcgtttctt ttctgtggct gcgtgaaagc cttaaagggc tccgggaggg ccctttgtgc    2400
105 gggggggagc ggctcggggg gtgcgtgcgt gtgtgtgtgc gtggggagcg ccgcgtgcgg    2460
107 cccgcgctgc ccggcggctg tgagcgctgc gggcgcggcg cggggctttg tgcgctccgc    2520
109 gtgtgcgcga ggggagcgcg gccggggggcg gtgccccgcg gtgcggggggg gctgcgaggg   2580
111 gaacaaaggc tgcgtgcggg gtgtgtgcgt ggggggggtga gcaggggtg tgggcgcggc    2640
113 ggtcgggctg taaccccccc ctgcacccce ctccccgagt tgctgagcac ggcccggctt    2700
115 cgggtgcggg gctccgtgcg gggcgtggcg cggggctcgc cgtgccgggc ggggggtggc     2760
117 ggcaggtggg ggtgccgggc ggggcggggc cgcctcgggc cggggagggc tcgggggagg    2820
119 ggcgcggcgg ccccggagcg ccggcggctg tcgaggcgcg gcgagccgca gccattgcct    2880
121 tttatggtaa tcgtgcgaga gggcgcaggg acttcctttg tcccaaatct ggcggagccg    2940
123 aaatctggga ggcgccgccg caccccctct agcgggcgcg ggcgaagcgg tgcggcgccg    3000
125 gcaggaagga aatgggcggg gagggccttc gtgcgtcgcc gcgccgccgt cccttctcc     3060
127 atctccagcc tcggggctgc cgcaggggga cggctgcctt cggggggggac ggggcagggc   3120
129 gggggttcggc ttctggcgtg tgaccggcgg ggtttatatc ttcccttctc tgttcctccg   3180
131 cagcccccaa gcttaaggtg cacggcccac gtggggacta gtgccacc atg gcg ctc     3237
132                                                       Met Ala Leu
133                                                        1
135 ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc acc aga agt     3285
136 Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu Thr Arg Ser
137      5                  10                  15
139 ttg agt atc act act cct gaa cag atg att gaa aag gcc aaa ggg gaa     3333
140 Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala Lys Gly Glu
141 20                  25                  30                  35
143 act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa gac cag ggg     3381
144 Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu Asp Gln Gly
145                  40                  45                  50
147 ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat cag aag gtg     3429
148 Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn Gln Lys Val
149                  55                  60                  65
151 gat caa gtg att att tta tat tct gga gac aaa att tat gac gac tac     3477
152 Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr Asp Asp Tyr
153             70                  75                  80
155 tac caa gat ctg aaa gga cga gta cat ttt aca agt aat gat ctc aaa     3525
156 Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn Asp Leu Lys
157             85                  90                  95
159 tca ggt gat gca tca ata aat gta aca aat cta cag ttg tca gat att     3573
160 Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu Ser Asp Ile
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Input Set : A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt
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161 100                   105                  110                 115
163 ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt gga aat aag    3621
164 Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val Gly Asn Lys
165                   120                  125                 130
167 aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca aga tgt tat    3669
168 Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr Arg Cys Tyr
169                   135                  140                 145
171 gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta aaa tgt gaa    3717
172 Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu Lys Cys Glu
173           150                  155                 160
175 cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag aaa ttg tcc    3765
176 Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln Lys Leu Ser
177       165                  170                 175
179 aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg act tca cct    3813
180 Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met Thr Ser Pro
181 180                   185                  190                 195
183 gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg aca tac agc    3861
184 Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly Thr Tyr Ser
185                   200                  205                 210
187 tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg ctt cgc ctg    3909
188 Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu Leu Arg Leu
189           215                  220                 225
191 gat gtg gtt cct cct tca aat aga gct gga aca att gca gga gct gtt    3957
192 Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala Gly Ala Val
193           230                  235                 240
195 ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt atc atc ttt tgc    4005
196 Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile Ile Phe Cys
197       245                  250                 255
199 tgt cgt taa tctagataag taatgatcat aatcagccat atcacatctg           4054
200 Cys Arg
201 260
203 tagaggtttt acttgcttta aaaaacctcc cacacctccc cctgaacctg aaacataaaa  4114
205 tgaatgcaat tgttgttgtt aacttgttta ttgcagctta taatggttac aaataaagca  4174
207 atagcatcac aaatttcaca aataaagcat tttttcact gcattctagt tgtggtttgt   4234
209 ccaaactcat caatgtatct tatcatgtct ggatccccgg gtaccgagct cg          4286
212 <210> SEQ ID NO: 2
213 <211> LENGTH: 261
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial/Unknown
217 <220> FEATURE:
217 <223> OTHER INFORMATION:
217 <400> SEQUENCE: 2
219 Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu
220 1                 5                    10                  15
223 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
224                   20                   25                  30
227 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
228           35                   40                  45
231 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
```

Erra
— See explanation on p. 6

C--> 215
W-(> 217
W--> 217

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Input Set : A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt
Output Set: N:\CRF3\06272002\I899634B.raw

```
232     50                    55                    60
235 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
236 65                    70                    75                    80
239 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
240                    85                    90                    95
243 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
244                    100                   105                   110
247 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
248          115                   120                   125
251 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
252     130                   135                   140
255 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
256 145                   150                   155                   160
259 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
260                    165                   170                   175
263 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
264                    180                   185                   190
267 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
268          195                   200                   205
271 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
272     210                   215                   220
275 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
276 225                   230                   235                   240
279 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
280                    245                   250                   255
283 Ile Phe Cys Cys Arg
284                    260
287 <210> SEQ ID NO: 3
288 <211> LENGTH: 1098
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial/Unknown
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(1098)
295 <223> OTHER INFORMATION: full length porcine CAR
298 <400> SEQUENCE: 3
299 atg gcg ctc ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc     48
300 Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu
301 1               5                   10                  15
303 acc aga agt ttg agt atc act act cct gaa cag atg att gaa aag gcc     96
304 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
305          20                  25                  30
307 aaa ggg gaa act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa    144
308 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
309          35                  40                  45
311 gac cag ggg ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat    192
312 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
313     50                  55                  60
315 cag aag gtg gat caa gtg att att tta tat tct gga gac aaa att tat    240
```

C--> 290 on line marked in original.

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316 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
317 65                  70                  75                  80
319 gac gac tac tac caa gat ctg aaa gga cga gta cat ttt aca agt aat      288
320 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
321                     85                  90                  95
323 gat ctc aaa tca ggt gat gca tca ata aat gta aca aat cta cag ttg      336
324 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
325                     100                 105                 110
327 tca gat att ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt      384
328 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
329             115                 120                 125
331 gga aat aag aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca      432
332 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
333         130                 135                 140
335 aga tgt tat gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta      480
336 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
337 145                 150                 155                 160
339 aaa tgt gaa cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag      528
340 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
341                 165                 170                 175
343 aaa ttg tcc aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg      576
344 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
345             180                 185                 190
347 act tca cct gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg      624
348 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
349         195                 200                 205
351 aca tac agc tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg      672
352 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
353 210                 215                 220
355 ctt cgc ctg gat gtg gtt cct cct tca aat aga gct gga aca att gca      720
356 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
357 225                 230                 235                 240
359 gga gct gtt ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt att      768
360 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
361             245                 250                 255
363 gtg ttt tgc tgt cat aaa aag cgc aga gaa gaa aaa tac gaa aaa gaa      816
364 Val Phe Cys Cys His Lys Lys Arg Arg Glu Glu Lys Tyr Glu Lys Glu
365         260                 265                 270
367 gtg cat cat gat atc agg gaa gac gtg cct cct ccg aag agc aga acg      864
368 Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr
369         275                 280                 285
371 tcc act gcc aga agc tac ctc ggc agc aac cac tcg tcc ctg gga tcc      912
372 Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser
373     290                 295                 300
375 atg tct cct tcc aac atg gaa ggc tat tcc aag act cag tat aac cag      960
376 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln
377 305                 310                 315                 320
379 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg      1008
380 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/27/2002
PATENT APPLICATION: US/09/899,634B   TIME: 13:06:29

Input Set : A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt
Output Set: N:\CRF3\06272002\I899634B.raw

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)
Seq#:2,4

VERIFICATION SUMMARY   DATE: 06/27/2002
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L:9   M:270 C: Current Application Number differs, Replaced Current Application No
L:9   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:217 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:217 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:290 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:395 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:397 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:397 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:494 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:509 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:524 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:539 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:554 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:569 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:584 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:599 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
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